

rnpsn-2

GenCore version 6.2
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2007, 23:17:57 ; Search time 238 Seconds
(without alignments)
1109.272 Million cell updates/sec

Title: US-10-534-978A-2
Perfect score: 68
Sequence: 1 aatccgtcgcagcagagtttag.....agggttaggggttaggggttag 68

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4240741 seqs, 1941225641 residues

Total number of hits satisfying chosen parameters: 8481482

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
11: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%		Query			ID	Description
Result	No.	Score	Match	Length	DB			
c	1	68	100.0	68	6	US-10-534-978A-2	Sequence 2, Appli	
	2	55.4	81.5	210920	6	US-10-540-898-99	Sequence 99, Appl	
c	3	54.8	80.6	1000	8	US-11-266-748A-283486	Sequence 283486,	
	4	54.8	80.6	1000	8	US-11-266-748A-310126	Sequence 310126,	
c	5	54.8	80.6	1000	8	US-11-266-748A-393223	Sequence 393223,	
	6	54.8	80.6	1000	8	US-11-266-748A-483941	Sequence 483941,	

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OM nucleic - nucleic search, using sw model

Run on: January 31, 2007, 23:16:49 ; Search time 1548 Seconds
(without alignments)
539.767 Million cell updates/sec

Title: US-10-534-978A-2
Perfect score: 68
Sequence: 1 aatccgtcgagcagagtttag.....agggttaggggttaggggttag 68

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	62	91.2	62	8 US-10-712-672-5573	Sequence 5573, Ap

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OM nucleic - nucleic search, using sw model

Run on: January 31, 2007, 23:13:10 ; Search time 162 Seconds
(without alignments)
785.404 Million cell updates/sec

Title: US-10-534-978A-2
Perfect score: 68
Sequence: 1 aatccgctcgagcagagtttag.....agggttagggtttagggtttag 68

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : Issued Patents_NA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	62	91.2	62	2	US-08-632-662A-19	Sequence 19, Appl
2	62	91.2	62	2	US-08-482-132A-14	Sequence 14, Appl
3	62	91.2	62	2	US-08-631-554A-19	Sequence 19, Appl
4	62	91.2	62	2	US-09-100-153-19	Sequence 19, Appl
5	60.4	88.8	62	3	US-08-974-549A-619	Sequence 619, App
6	60.4	88.8	62	3	US-08-912-951-329	Sequence 329, App
7	60.4	88.8	62	3	US-09-402-181B-619	Sequence 619, App

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OM nucleic - nucleic search, using sw model

Run on: January 31, 2007, 22:28:57 ; Search time 5212 Seconds
(without alignments)
809.438 Million cell updates/sec

Title: US-10-534-978A-2
Perfect score: 68
Sequence: 1 aatccgctcgagcagagtttag.....agggttaggggttaggggttag 68

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_est13:*
12: gb_est12:*
13: gb_est11:*
14: gb_est10:*
15: gb_gss1:*
16: gb_gss2:*
17: gb_gss3:*
18: gb_gss4:*
19: gb_gss5:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%
Result Query

rst-2

No.	Score	Match	Length	DB	ID	Description
c 1	57.2	84.1	430	18	DX787013	DX787013 2687890 V
c 2	56.8	83.5	975	18	CW924439	CW924439 EDCB443TR
c 3	56.4	82.9	471	15	AZ775262	AZ775262 2M0007D01
c 4	56.4	82.9	934	19	CR113335	CR113335 Forward s
c 5	56.2	82.6	550	3	BI786967	BI786967 sai55e09.
6	56.2	82.6	1039	19	CNS02UID	AL214510 Tetraodon
7	56.2	82.6	1055	19	CNS02VFA	AL215695 Tetraodon
8	56	82.4	278	16	BZ230619	BZ230619 CH230-426
c 9	56	82.4	412	17	CE481345	CE481345 tigr-gss-
c 10	56	82.4	617	16	CE125880	CE125880 tigr-gss-
c 11	56	82.4	940	18	DU752273	DU752273 ASNF2495.
c 12	55.8	82.1	250	17	CE822593	CE822593 tigr-gss-
c 13	55.8	82.1	752	19	CNS0525K	AL317729 Tetraodon
c 14	55.8	82.1	936	18	DU760955	DU760955 ASNG3439.
15	55.6	81.8	99	3	BJ014554	BJ014554 BJ014554
c 16	55.6	81.8	226	17	CE266979	CE266979 tigr-gss-
c 17	55.6	81.8	354	17	CW625529	CW625529 Ggal_34_U
c 18	55.6	81.8	497	18	DX794125	DX794125 2629234 V
c 19	55.6	81.8	500	18	DX766113	DX766113 2700494 V
c 20	55.6	81.8	578	19	LBAF055E09	BX541447 Leishmani
c 21	55.6	81.8	937	18	DU745259	DU745259 ASNC2695.
c 22	55.6	81.8	994	18	DU737833	DU737833 APKI4419.
c 23	55.4	81.5	87	18	DX773541	DX773541 2638389 V
c 24	55.4	81.5	151	15	AZ213114	AZ213114 Sheared D
c 25	55.4	81.5	153	17	CE606025	CE606025 tigr-gss-
c 26	55.4	81.5	165	18	DX655407	DX655407 2275293 V
c 27	55.4	81.5	166	18	DX779785	DX779785 2568866 V
c 28	55.4	81.5	171	17	CE806145	CE806145 tigr-gss-
c 29	55.4	81.5	175	16	CE041073	CE041073 tigr-gss-
c 30	55.4	81.5	181	17	CE383249	CE383249 tigr-gss-
c 31	55.4	81.5	189	18	DX766901	DX766901 2569194 V
c 32	55.4	81.5	203	16	CE181028	CE181028 tigr-gss-
c 33	55.4	81.5	206	17	CE285245	CE285245 tigr-gss-
c 34	55.4	81.5	212	18	DX959239	DX959239 CHORI105-
c 35	55.4	81.5	215	18	DX938281	DX938281 CHORI105-
c 36	55.4	81.5	216	18	DX646671	DX646671 2261399 V
c 37	55.4	81.5	217	17	CE560550	CE560550 tigr-gss-
c 38	55.4	81.5	219	16	CE166161	CE166161 tigr-gss-
c 39	55.4	81.5	242	17	CE824278	CE824278 tigr-gss-
c 40	55.4	81.5	253	17	CE503885	CE503885 tigr-gss-
c 41	55.4	81.5	260	17	CE249756	CE249756 tigr-gss-
c 42	55.4	81.5	266	17	CE462746	CE462746 tigr-gss-
c 43	55.4	81.5	281	18	DX770418	DX770418 2263546 V
c 44	55.4	81.5	286	18	DX722396	DX722396 2312598 V
c 45	55.4	81.5	290	15	AQ948278	AQ948278 Sheared D
c 46	55.4	81.5	299	17	CE513787	CE513787 tigr-gss-
c 47	55.4	81.5	303	18	DX777808	DX777808 2632848 V
c 48	55.4	81.5	314	16	CE169776	CE169776 tigr-gss-
c 49	55.4	81.5	322	18	DX789839	DX789839 2628394 V
c 50	55.4	81.5	324	18	DX765215	DX765215 2661801 V
c 51	55.4	81.5	326	16	CE056399	CE056399 tigr-gss-
c 52	55.4	81.5	329	18	DX795742	DX795742 2690845 V
c 53	55.4	81.5	332	16	CE005651	CE005651 tigr-gss-
c 54	55.4	81.5	337	18	DX680285	DX680285 2434812 V
c 55	55.4	81.5	345	18	DX791550	DX791550 2690054 V

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OM nucleic - nucleic search, using sw model

Run on: January 31, 2007, 22:09:00 ; Search time 565 Seconds
(without alignments)
891.891 Million cell updates/sec

Title: US-10-534-978A-2
Perfect score: 68
Sequence: 1 aatccgtcgagcagagtttag.....agggttagggtttagggtttag 68

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : N_Geneseq_200701:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*
16: geneseqn2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					Description
Result	Query	Match	Length	DB	ID		
No.	Score						
1	68	100.0	68	6	ABK10341		Abk10341 Zinc fing

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OM nucleic - nucleic search, using sw model

Run on: January 31, 2007, 22:15:44 ; Search time 2750
Seconds

(without alignments)
1709.156 Million cell

updates/sec

Title: US-10-534-978A-2
Perfect score: 68
Sequence: 1
aatccgtcgagcagagtttag.....agggttaggggttaggggttag 68

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to
have a
score greater than or equal to the score of the result being
printed,
and is derived by analysis of the total score distribution.

SUMMARIES

rge-2

Result	Query					
No.	Score	Match	Length	DB	ID	
Description	-----					
1	68	100.0	68	2	CQ818437	
CQ818437 Sequence						
2	68	100.0	68	2	AX395585	
AX395585 Sequence						
3	62	91.2	62	2	AR037864	
AR037864 Sequence						
4	62	91.2	62	2	AR054745	
AR054745 Sequence						
5	62	91.2	62	2	AR069397	
AR069397 Sequence						
6	62	91.2	62	2	AX395632	
AX395632 Sequence						
7	60.4	88.8	62	2	AX810663	
AX810663 Sequence						
8	60.4	88.8	62	2	BD011314	
BD011314 Human tel						
9	60.4	88.8	62	2	AR243525	
AR243525 Sequence						
10	60.4	88.8	62	2	E37063	E37063
Human telom						
11	60.4	88.8	62	2	AR390731	
AR390731 Sequence						
12	60.4	88.8	62	2	AR393345	
AR393345 Sequence						
c 13	59	86.8	202030	12	AC112339	
AC112339 Rattus no						
c 14	59	86.8	301416	12	AC120690	
AC120690 Rattus no						
15	58.8	86.5	257941	12	AC131474	
AC131474 Rattus no						
16	58.4	85.9	124032	12	AC182354	
AC182354 Loxodonta						
17	58.4	85.9	185017	12	AC130953	
AC130953 Rattus no						
18	58.4	85.9	212491	6	AC105470	
AC105470 Rattus no						
c 19	58.4	85.9	257714	12	AC096219	
AC096219 Rattus no						
20	58.2	85.6	191168	12	AC099193	
AC099193 Rattus no						
c 21	58.2	85.6	260648	12	AC117966	
AC117966 Rattus no						
c 22	58	85.3	37174	4	AC151924	
AC151924 Phaeodact						
c 23	57.2	84.1	148	2	AR171834	
AR171834 Sequence						
c 24	57.2	84.1	148	2	AR351437	
AR351437 Sequence						
c 25	57.2	84.1	148	2	I95605	I95605
Sequence 20						
c 26	57.2	84.1	110000	12	AC110838_1	
Continuation (2 of						